The tooth enamel protein, porcine amelogenin, is an intrinsically disordered protein with an extended molecular configuration in the monomeric form. Supporting Information.

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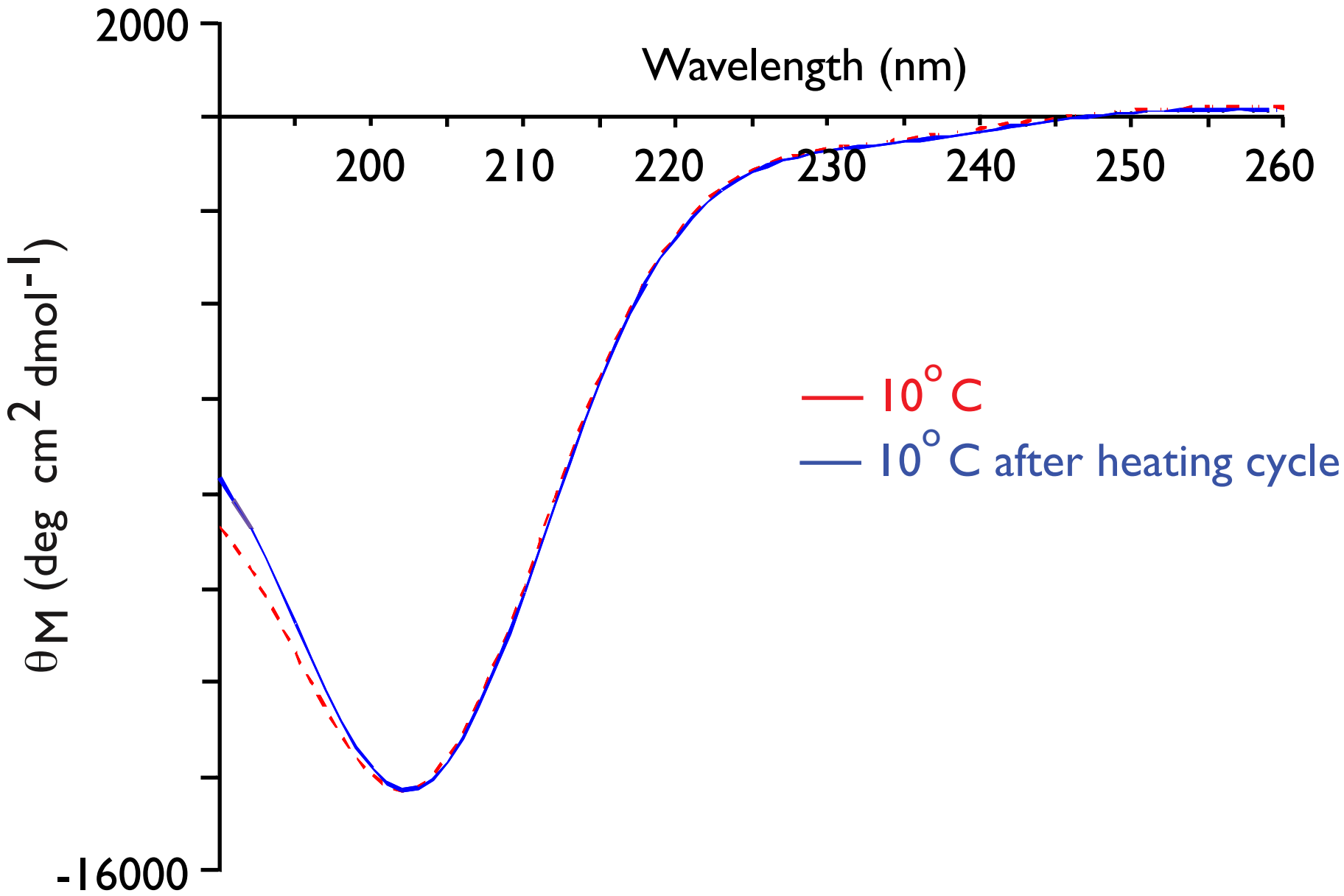
Supporting Figure S1: *Unquenched and quenched CD spectra of rP172 in UDDW.* Both spectra were recorded at 10° C with identical acquisition parameters. The red curve is the initial spectra of the sample ("unquenched"), the blue curve is the spectra obtained at 10° C after the initial sample was heated up up to 85° C, with subsequent cooling down to 10° C ("quenched"). The "quenched" spectrum is reproducible within the experimental error and indicates the absence of aggregation.


2000
Wavelength (nm)
200
210
220
230
240
250
260
θM (deg cm2 dmol-1)
-16000
10° C
10° C after heating cycle

Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
P2	---	62.42	176.63	31.86	27.01	---	---	---	---	4.38	2.29	1.86	---	---
L3	124.20	52.87	177.07	41.41	---	---	---	---	8.42	3.97	---	---	---	7.8
P4	---	63.51	177.7	31.99	27.82	---	---	---	---	4.36	2.29	---	---	---
P5	---	63.51	177.7	31.99	27.82	---	---	---	---	4.36	2.29	---	---	---
H6	118.3	53.30	172.42	28.68	---	---	---	---	8.30	4.53	3.09	---	---	9.4
P7	---	63.44	177.47	32.08	27.52	---	---	---	---	4.23	2.17	1.86	---	---
G8	109.6	44.90	173.43	---	---	---	---	---	8.59	3.85	---	---	---	8.3
H9	118.3	53.3	172.42	28.84	---	---	---	---	8.30	4.53	3.09	---	---	9.4
P10	---	63.62	177.38	32.07	27.72	---	---	---	---	4.36	2.24	1.84	---	---
G11	109.83	45.05	173.65	---	---	---	---	---	8.65	3.85	---	---	---	7.2
Y12	120.02	57.85	175.51	38.84	---	---	---	---	8.03	4.50	2.87	---	---	---
I13	123.71	60.66	175.00	38.90	17.1	39.22	12.81	---	8.03	3.97	1.58	0.60	1.27, 0.60	10.1
N14	122.48	52.86	174.64	38.84	---	---	---	---	8.34	4.55	2.66	---	---	---
F15	121.54	58.00	175.43	39.69	---	---	---	---	8.21	4.45	2.89, 2.83	---	---	8.2
S16	117.21	58.05	173.86	63.71	---	---	---	---	8.14	4.32	3.87, 3.72	---	---	7.9
Y17	121.80	58.01	175.60	38.55	---	---	---	---	8.07	4.42	2.91	---	---	9.1
E18	122.02	56.30	175.96	30.28	---	---	---	---	8.23	4.49	2.14	1.86	---	---
V19	121.59	62.40	176.08	32.45	24.94	23.3	---	---	8.14	3.99	---	0.85	---	---
L20	125.80	55.06	177.07	42.29	---	---	---	---	8.35	4.39	1.60	1.48	0.78	7.2
T21	116.58	60.33	172.85	69.48	---	---	---	---	8.00	4.03	3.77	---	---	8.7
P22	---	63.62	177.38	27.57	---	---	---	---	---	4.35	2.26	1.85	---	---
L23	121.93	56.01	177.96	41.05	---	---	---	---	8.14	4.23	1.57	0.82	---	---
K24	120.67	57.14	177.13	32.81	---	---	---	---	8.12	4.21	3.14	1.65	---	---
W25	120.91	58.78	176.70	29.40	---	---	---	---	8.09	4.50	3.15	---	---	---

Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
Y26	120.08	58.77	176.04	38.45	---	---	---	---	8.33	3.96	2.76	---	---	---
Q27	119.71	57.1	176.41	28.80	28.93	---	---	---	8.07	3.98	1.94	---	---	---
N28	117.75	54.04	175.51	38.46	---	---	---	---	8.18	4.50	2.72	---	---	7.8
M29	119.96	56.24	176.55	32.38	31.51	---	----	---	7.98	4.19	3.00	---	---	---
I30	120.24	61.62	176.23	38.05	27.10	13.01	---	---	8.03	3.97	1.58	0.60	---	---
R31	123.28	55.59	175.82	31.95	28.60	40.74	---	---	8.40	4.24	2.47	1.88	1.34	7.5
H32	119.47	52.98	172.03	28.57	---	---	---	---	8.38	4.53	3.09	---	---	---
P33	---	63.34	176.62	31.98	27.57	---	---	---	---	4.32	2.04	1.88	---	---
Y34	120.06	57.9	175.89	38.44	---	---	---	---	8.33	4.52	2.96	---	---	6.6
T35	115.66	61.4	174.00	70.09	21.27	---	---	---	7.93	4.03	3.77	---	---	9.2
S36	117.88	58.44	173.86	63.73	---	---	---	---	8.22	4.32	3.72	---	---	7.8
Y37	121.94	58.14	176.15	38.75	---	---	---	---	8.21	4.46	2.94, 2.84	---	---	---
G38	110.41	44.91	173.36	---	----	---	---	---	8.27	3.85	---	---	---	5.5
Y39	119.96	57.91	175.15	38.81	---	---	---	---	7.98	4.51	2.94	---	---	---
E40	N/O													---
c-P41	---	65.20	177.12	31.96	22.88	---	---	---	---	4.32	2.04	1.88	---	---
M42	120.32	56.07	177.08	31.96	---	---	---	---	8.53	4.25	2.47	1.96	---	---
G43	110.8	45.38	174.80	---	---	---	---	---	8.47	3.80	---	---	---	6.2
G44	108.71	45.10	174.07	---	---	---	---	---	8.20	4.01, 3.77	---	---	---	6.2
W45	120.06	57.71	176.72	29.4	---	---	---	---	8.09	4.50	3.15	---		6.2
L46	121.95	55.44	177.12	42.00	24.70	---	---	---	8.14	4.12	1.30	0.74	---	---
H47	117.83	55.06	174.11	28.63	---	---	---	---	8.29	4.53	3.09	---	---	9.3
H48	119.20	55.23	173.88	29.04	---	---	---	---	8.39	4.36	3.09	---	---	---

Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
I50	123.80	60.90	176.01	38.42	27.20	17.65	---	---	8.42	4.06	1.75	1.09	---	---
I51	128.18	60.90	174.29	38.42	27.20	17.65	---	---	8.39	4.06	1.75	1.09	---	9.4
c-P52	---	62.92	176.59	32.21	25.34	---	---	---	---	4.23	2.24	1.86	---	---
V53	121.59	62.30	176.59	32.72	20.89	---	---	---	8.32	4.02	1.97	0.85	---	---
V54*	121.30, 125.28	62.23	176.10	32.79	20.77	---	---	---	8.38	4.12	2.02	0.89	---	---
S55	120.42	58.29	174.57	63.77	---	---	---	---	8.51	4.39	3.80	---	---	6.8
Q56	122.76	55.83	175.84	29.45	33.66	30.63	---	---	8.56	4.30	2.31	1.86	---	8.2
Q57	121.86	55.64	175.95	29.48	33.79	29.49	---	---	8.52	4.33	2.31	2.01	---	---
T58	118.66	60.16	172.98	65.59	---	---	---	---	8.35	4.03	3.77	---	---	8.3
P59	---	63.47	177.08	32.08	27.57	---	---	---	---	4.35	2.26	1.85	---	---
Q60	120.74	55.94	176.20	29.38	29.17	---	---	---	8.58	4.23	2.34	1.96	---	---
S61	117.14	58.61	174.63	63.84	---	---	---	---	8.38	4.35	3.79	---	---	6.9
H62	120.66	55.09	174.01	29.00	---	---	---	---	8.58	4.66	3.23	---	---	---
A63*	124.71, 125.08	52.61	177.62	19.14	---	---	---	---	8.31	4.23	1.31	---	---	---
L64	121.81	54.95	177.29	42.18	27.09	24.69	23.55	---	8.35	4.33	1.56	0.86	---	7.3
Q65	122.51	53.64	173.87	28.89	29.20	---	---	---	8.44	4.23	2.25	1.88	---	---
P66	---	63.02	176.66	32.15	27.29	---	---	---	---	4.32	2.21	1.73	---	---
H67	118.55	55.19	174.28	29.02	---	---	---	---	8.68	4.57	3.11	---	---	7.6
H68	120.11	55.19	173.94	29.54	---	---	---	---	8.56	4.62	3.10	---	---	6.1
H69	121.48	55.35	173.98	29.25	---	---	---	---	8.78	4.61	3.10	---	---	8.0
I70	125.23	58.98	174.21	38.46	---	---	---	---	8.40	4.06	1.75	1.09	---	---
P71	---	63.04	176.55	32.17	27.29	---	---	---	---	4.32	2.21	1.73	---	---
M72	121.74	55.74	176.09	32.81	---	---	---	---	8.49	4.39	1.97	2.53	---	---
V73	124.00	59.79	174.31	32.71	---	---	---	---	8.32	4.12	2.02	0.89	---	7.8

Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
P74	---	63.14	176.51	32.14	27.34	---	---	---	---	4.35	2.26	1.90	---	---
A75	124.41	52.44	177.80	19.10	---	---	---	---	8.57	4.22	1.34	---	---	5.1
Q76	119.75	55.57	175.83	29.35	---	---	---	---	8.41	4.24	2.33	1.97	---	6.8
Q77	123.27	55.46	174.02	29.35	---	---	---	---	8.53	4.24	2.33	1.97	---	7.6
P78	---	63.32	177.35	32.13	27.71	---	---	---	---	4.39	2.26	1.91	---	---
G79	109.21	44.94	173.71	---	---	---	---	---	8.51	4.33, 3.88	---	---	---	5.8
I80	121.89	58.29	174.77	38.54	---	---	---	---	8.08	4.06	1.75	---	---	---
P81	---	63.23	176.77	32.07	27.47	---	---	---	---	4.33	2.26	1.93	---	---
Q82	121.11	55.67	175.92	33.91	29.49	---	---	---	8.57	4.26	2.30	1.86	1.63	7.0
Q83	123.36	53.92	173.88	28.97	---	---	---	---	8.54	4.26	2.30	1.86	1.63	7.2
P84	---	63.04	176.55	32.17	27.47	---	---	---	---	4.33	2.26	1.93	---	---
M85	121.74	55.74	176.09	32.81	---	---	---	---	8.49	4.39	1.97	2.53	---	---
M86	121.74	55.74	176.09	32.81	---	---	---	---	8.49	4.39	1.97	2.53	---	---
P87	---	62.42	176.63	31.86	27.01	---	---	---	---	4.39	2.26	1.93	---	---
L88	123.94	52.87	177.29	41.41	27.09	---	---	---	8.42	4.33	1.56	0.86	---	7.8
P89	---	63.51	177.70	31.99	27.82	---	---	---	---	4.36	2.29	1.93	---	---
G90	109.40	45.15	174.20	---	---	---	---	---	8.56	4.32, 3.88	---	---	---	7.9
Q91	119.51	55.72	175.97	33.67	29.01	---	---	---	8.17	4.25	2.27	1.97	---	8.0
H92	119.75	55.72	174.31	29.13	---	---	---	---	8.68	4.71	3.18	---	---	9.1
S93	117.27	58.43	174.45	63.74	---	---	---	---	8.46	4.41	3.81	---	---	7.3
M94	122.70	55.19	176.22	32.79	---	---	---	---	8.66	4.55	2.57	2.00	---	8.3
T95	118.71	60.12	172.87	69.59	---	---	---	---	835	4.31	4.10	1.12	---	8.5
c-P96	---	63.31	177.11	32.20	25.09	---	---	---	---	4.44	2.28	1.88	---	---
T97	115.18	62.18	174/49	69.70	---	---	---	---	8.33	4.31	4.10	1.12	---	8.4

Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
Q98	122.83	55.58	175.58	29.55	29.36	---	---	---	8.42	4.24	2.27	1.91	---	7.8
H99	120.04	55.58	174.07	29.13	---	---	---	---	8.64	4.60	3.11	---	---	8.8
H100	122.30	55.38	173.99	29.22	---	---	---	---	8.67	4.60	3.11	---	---	---
Q101	122.30	55.23	175.46	29.72	33.53	---	---	---	8.49	4.35	2.22	2.55, 1.88	---	---
P102	---	63.18	176.02	32.03	---	---	---	---	---	4.36	2.24	1.83	---	---
N103	118.76	53.15	174.72	38.82	---	---	---	---	8.58	4.61	2.72	---	---	---
L104	124.03	53.02	174.97	41.92	---	---	---	---	8.22	4.33	1.56	0.86	---	8.3
P105	---	62.42	176.63	31.86	27.01	---	---	---	---	4.38	2.24	1.83	---	---
L106	123.94	52.87	174.97	41.41	---	---	---	---	8.42	4.38	1.56	0.86	---	7.8
P107	---	63.14	176.51	32.14	27.34	---	---	---	---	4.35	2.26	1.90	---	---
A108	124.41	52.44	177.80	19.10	---	---	---	---	8.57	4.22	1.34	---	---	5.1
Q109	119.75	53.81	175.92	28.91	29.35	---	---	---	8.41	4.24	2.33	1.97	---	6.8
Q110	123.36	55.66	174.02	28.86	29.35	---	---	---	8.53	4.24	2.33	1.97	---	7.6
P111	---	63.27	176.39	32.15	27.21	---	---	---	---	4.42	2.51	2.03	---	---
F112	120.85	57.79	175.26	39.56	---	---	---	---	8.37	4.49	2.91	---	---	---
Q113	124.58	55.63	172.97	29.81	---	---	---	---	8.17	4.28	2.35	1.99	---	---
P114	---	63.12	176.80	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---
Q115	120.94	55.63	175.91	32.28	---	---	---	---	8.60	4.28	2.35	1.99	---	---
P116	---	63.12	176.80	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---
V117	124.00	62.29	176.20	31.70	20.89	---	---	---	8.32	4.00	1.97	0.90	---	---
Q118	126.03	53.52	173.88	28.97	---	---	---	---	8.59	4.28	2.35	1.99	---	7.7
P119	---	63.12	176.80	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---
Q120	120.94	55.63	175.91	32.28	---	---	---	---	8.60	4.28	2.35	1.99	---	7.7
P121	--	63.12	176.08	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---

Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
H122	120.69	55.38	173.99	29.22	---	---	---	---	8.67	4.60	3.11	---	---	---
Q123	122.30	55.23	175.46	29.72	---	---	---	---	8.49	4.35	2.22	2.55, 1.88	---	---
P124	---	63.12	176.80	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---
L125	123.65	41.83	174.91		---	---	---	---	8.31	4.38	1.56	0.86	---	---
Q126	N/O													
P127	---	63.12	176.80	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---
Q128	120.95	55.69	175.90	29.60	---	---	---	---	8.62	4.28	2.35	1.99	---	7.3
S129	117.17	63.21	176.63	32.82	---	---	---	---	8.50	4.26	3.77	---	---	---
c-P130	---	63.21	176.63	32.97	25.09	---	---	---	---	4.41	2.26	1.92	---	---
M131	120.93	56.07	175.96	32.81	29.79	19.5	---	---	8.54	4.30	2.29	1.94	---	---
H132	N/O													
t-P133	---	63.09	176.82	32.20	29.74	---	---	---	---	4.28	2.30	1.90	---	---
I134	121.99	61.20	176.25	38.68	27.27	17.65	13.75	---	8.47	4.09	1.78	1.17	---	---
Q135	126.11	53.38	173.71	28.97	---	---	---	---	8.52	4.28	2.35	1.99	---	---
P136	---	62.94	176.64	32.37	27.24	---	---	---	---	4.58	2.68	---	---	---
L137	120.67	55.14	177.10	42.34	27.00	24.57	---	---	8.47	4.27	1.56	0.87	---	---
L138	124.85	54.97	175.02	42.23	---	---	---	---	8.28	4.27	1.56	0.87	---	---
P139	---	63.12	176.80	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---
Q140	120.94	55.63	175.91	32.28	---	---	---	---	8.52	4.28	2.35	1.99	---	---
P141	---	63.12	176.80	32.05	27.21	---	---	---	---	4.36	2.28	1.87	---	---
P142	---	62.42	176.63	31.86	27.01	---	---	---	---	4.38	2.28	1.87	---	---
L143	123.94	52.87	175.02	41.41	---	---	---	---	8.42	4.27	1.56	0.87	---	7.8
P144	---	63.14	176.51	32.14	27.34	---	---	---	--	4.35	2.26	1.90	---	---
P145	---	63.21	176.63	32.82	27.09	---	---	---	---	4.41	2.26	1.92	---	---

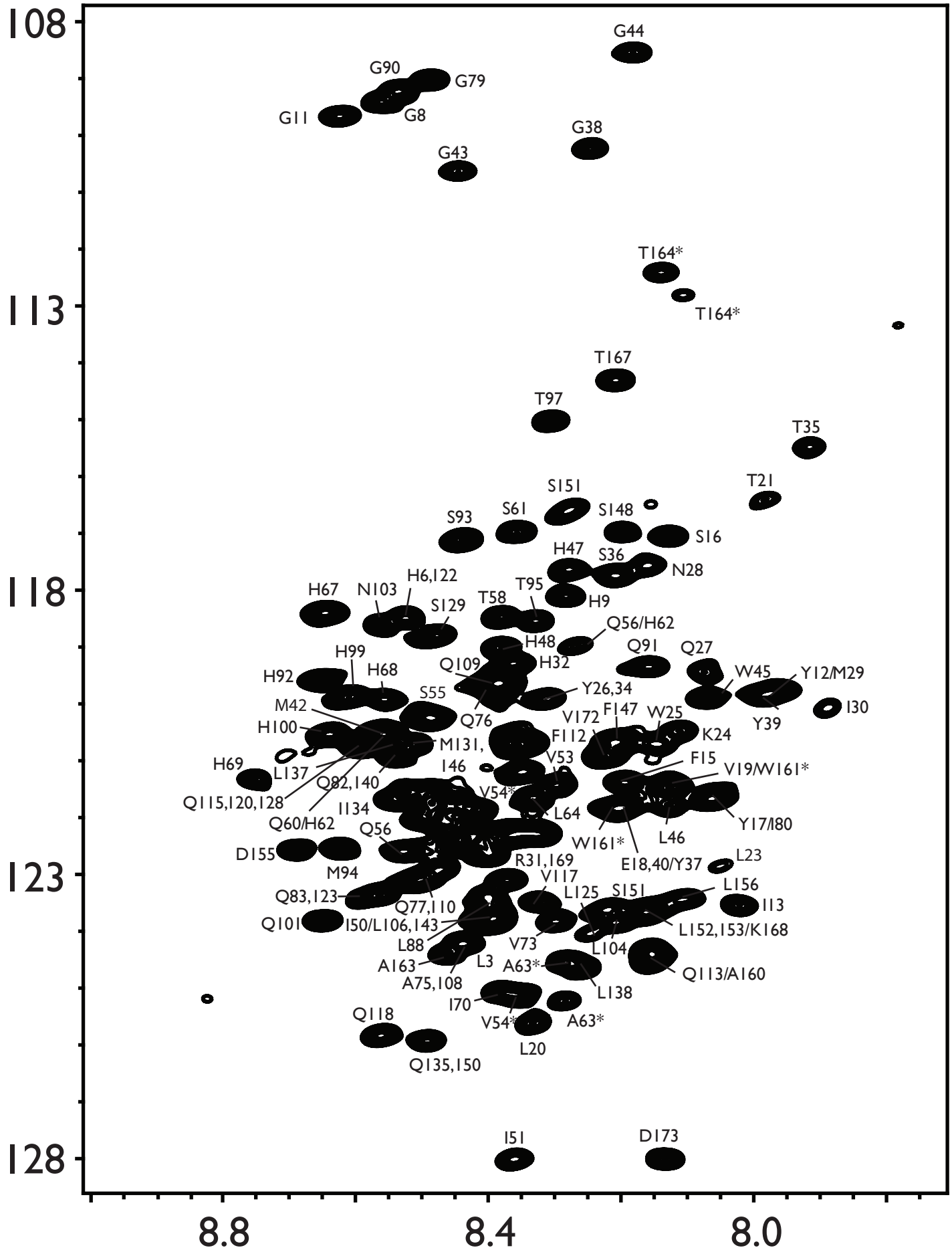
Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
M146	120.93	56.07	175.96	32.81	29.79	19.50	---	---	8.54	4.30	2.29	1.94	---	---
F147	120.83	57.83	175.58	39.70	---	---	---	---	8.25	4.57	3.03	---	6.75	
S148	117.17	58.02	174.43	63.88	---	---	---	---	8.22	4.26	3.77	---	---	8.0
M149	122.41	56.07	175.96	32.81	---	---	---	---	8.44	4.30	2.29	---	---	---
Q150	126.04	59.30	176.66	59.30	33.64	---	---	---	8.52	4.25	2.3	2.0	---	8.0
S151	116.80	58.54	174.24	63.63	---	---	---	---	8.30	4.62	3.77	---	---	7.8
L152	123.85	55.12	177.04	42.24	25.06	23.30	21.53	26.83	8.18	4.27	1.56	0.87	---	---
L153	123.85	52.87	175.06	41.64	25.06	23.30	21.53	26.83	8.18	4.27	1.56	0.87	---	---
c-P154	---	62.1	172.42	32.43	26.38	---	---	---	---	4.35	2.40	1.99	---	---
D155	122.76	53.47	178.65	41.30	---	---	---	---	8.72	4.53	2.59	---	---	6.7
L156	123.63	53.00	175.04	41.77	---	---	---	---	8.12	4.27	1.56	0.87	---	8.0
P157	---	63.02	176.82	32.04	27.21	---	---	---	---	3.98	2.25	1.86	---	---
L158	122.41	55.17	177.55	42.30	---	---	---	---	8.34	4.42	1.59	0.85	---	---
E159	121.48	56.04	175.51	29.93	---	---	---	---	8.39	4.15	2.19	1.83		7.7
A160	124.60	52.56	176.90	19.39	---	---	---	---	8.17	4.21	1.21	---	---	---
W161*	121.50, 121.67	55.02	174.30	28.94	---	---	---	---	8.14, 8.20	4.50	3.15	---	---	---
P162	---	63.38	176.72	32.06	27.24				---	4.34	2.25	1.86	---	---
A163	124.60	52.64	178.21	19.13	---	---	---	---	8.47	4.32	1.39		---	---
T164*	112.57, 112.83	61.76	174.36	69.84	---	---	---	---	8.15, 8.09	4.33	4.15	1.19	---	8.6
D165	122.39	54.18	176.65	40.81	---	---	---	---	8.37	4.58	2.68		---	---
K166	122.58	56.63	177.10	32.57	29.01	24.81	---	---	8.47	4.28	1.90	1.75, 1.40	---	---
T167	114.47	62.67	174.68	69.59	---	---	---	---	8.23	4.17	1.21	---	---	8.0
K168	123.84	56.20	176.32	32.85	28.97	24.65	---	---	8.18	4.25	1.77	1.32	---	---

Residue	N_{alpha}	C_{alpha}	C=O	C_{beta}	C_{gamma}	C_{delta}	$C_{epsilon}$	C_{other}	NH	H_{alpha}	H_{beta}	H_{gamma}	H_{other}	^{3}J
R169	123.28	56.02	176.17	30.81	42.76	27.21	---	---	8.40	4.30	2.30	1.97	1.86, 1.61	7.5
E170	122.14	56.11	176.11	29.81	---	---	---	---	8.53	4.26	2.25	1.94	---	6.8
E171	122.06	56.23	175.92	29.83	---	---	---	---	8.45	4.30	2.26	1.92	---	---
V172	121.09	61.99	175.06	32.93	---	---	---	---	8.24	4.14	2.07	0.88	---	8.6
D173	128.18	---	179.89	---	---	---	---	---	8.14	---	---	---	---	---

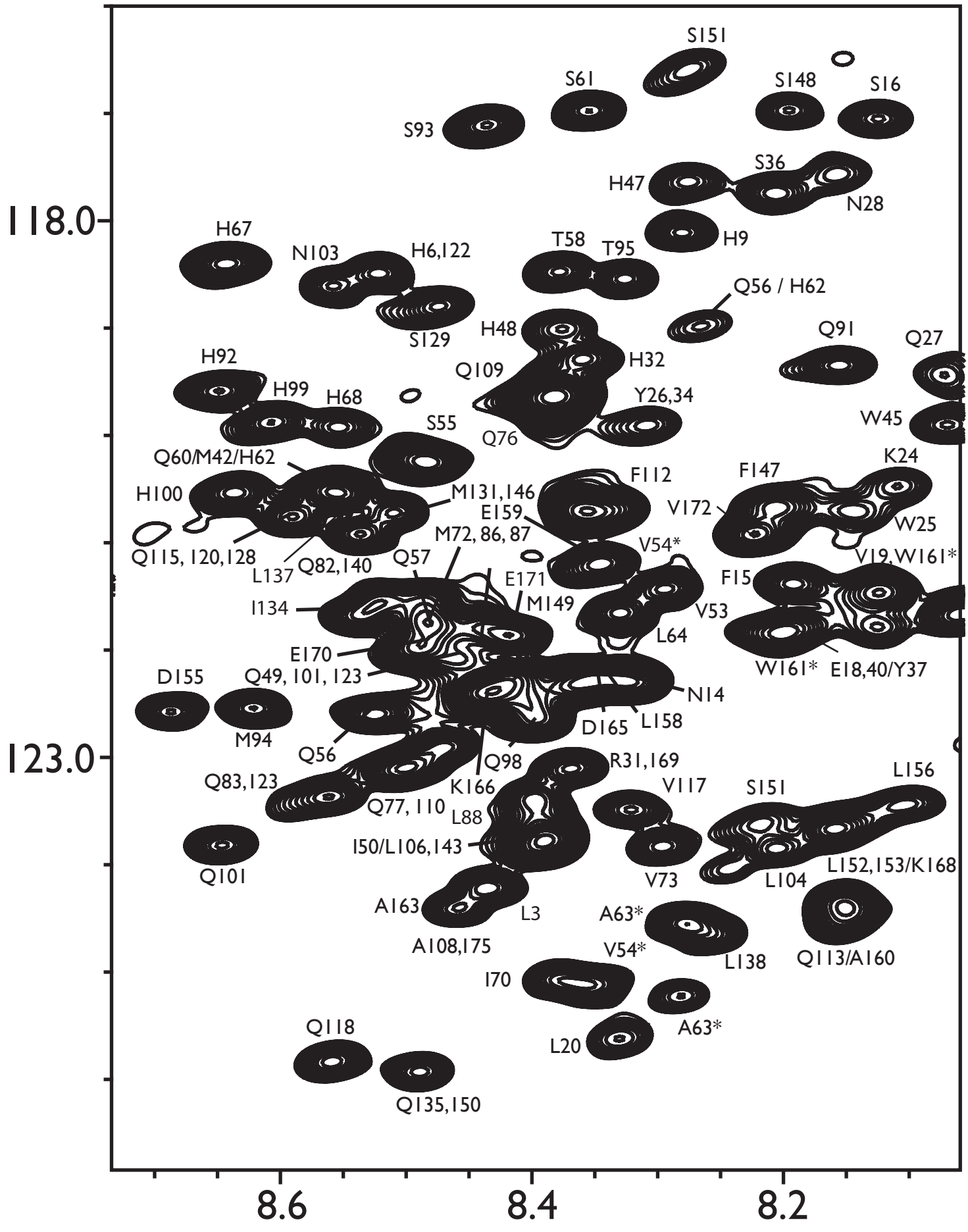
Table S1: Temperature-corrected 15-N, 13-C, 1-H backbone, sidechain chemical shifts for 75 micromolar rP172 in UDDW, pH 3.8, 283 K (1-H 700 MHz)

All chemical shifts in ppm, ^{3}J in Hz (obtained from HNHA experiments). Asterisk denotes residue with two crosspeaks on ^{15}H-^{1}H HSQC spectra identified in conformational exchange. N/O = not observed. Due to chemical shift overlap or other factors, sidechain ^{13}C and ^{1}H and ^{3}J were not detected and thus could not be assigned; these are denoted by "---". "Other" refers to higher order aliphatic, aromatic carbon or proton resonances beyond the gamma position. Where noted, certain Pro residues are categorized as the cis ("c") or trans ("t") configuration based upon database values for Pro $^{13}Cbeta$, $^{13}Cgamma$ chemical shifts. Note that the M1 residue is absent in recombinant rP172.

Supporting Figure S2: *Heteronuclear ^{1}H-^{15}N HSQC spectrum of amelogenin rP172 in unbufferred deionized distilled water (UDDW).* Spectra were obtained with 8 scans per increment, 1024 points in ω_2 (^{1}H) , 256 increments in ω_1 (^{15}N), a recovery delay of 1 sec, a spectral window of 12 ppm in ω_2 and 24 ppm in ω_1. Pulse widths were 8.62 µsec at -5 dB on the ^{1}H channel and 38 µsec at -2 dB on the ^{15}N channel. Decoupling was performed during acquisition using the GARP decoupling pulse train. Z-axis gradient parameters were of the sine.100 type. A sine-squared apodization function was used during processing. The size of the spectrum was 4096 by 1024 points, with zero-filling in both dimensions. The "*" symbol denotes duplicated HSQC resonances (V54, A63, W161, T164) that arise from conformational exchange.


108
113
118
123
128
8.8
8.4
8.0
G44
G90
G79
G11
G8
G38
G43
T164*
T164*
T167
T97
T35
T21
S151
S93
S61
S148
S16
H47
S36
N28
H6,122
H67
N103
T95
H9
T58
S129
Q56/H62
H48
Q91
Q27
H99
Q109
H32
W45
Y12/M29
H92
H68
S55
Y26,34
I30
M42
Q76
V172
F147
W25
Y39
H100
F112
K24
M131,
H69
L137
I46
V53
F15
V19/W161*
Q82,140
Q115,120,128
V54*
I134
L64
Y17/I80
Q60/H62
Q56
W161*
L46
D155
R31,169
E18,40/Y37
L23
M94
V117
L125
S151
L156
Q83,123
Q77,110
I13
Q101
I50/L106,143
L152,153/K168
L88
V73
L104
A163
L3
A63*
Q113/A160
A75,108
L138
I70
Q118
V54*
A63*
L20
Q135,150
I51
D173

Supporting Figure S3: *Expansion plot of the heteronuclear ^{1}H-^{15}N HSQC spectrum of amelogenin rP172 in UDDW.* Acquisition and processing parameters are identical to that described in Figure S2. The "*" symbol denotes duplicated HSQC resonances that are due to conformational exchange.


S151
S61
S148
S16
S93
S36
H47
N28
H9
H67
N103
H6,122
T58
T95
Q56 / H62
S129
H48
Q91
Q27
H92
Q109
H32
H99
H68
Y26,34
W45
S55
Q76
Q60/M42/H62
F112
F147
K24
H100
M131,146
V172
E159
W25
M72, 86, 87
V54*
Q115, 120,128
L137
Q82,140
Q57
E171
V19,W161*
F15
I134
M149
V53
L64
E170
W161*
E18,40/Y37
D155
Q49, 101, 123
N14
M94
D165
L158
Q56
Q98
R31,169
L156
Q83,123
K166
V117
S151
Q77, 110
L88
I50/L106,143
V73
L104
L152,153/K168
Q101
A163
L3
A63*
A108,175
V54*
L138
Q113/A160
I70
A63*
Q118
L20
Q135,150
118.0
123.0
8.6
8.4
8.2